From:	Chan, Christina
Sent:	Wednesday, February 01, 2006 10:41 AM
To:	Sullivan, Daniel; STIC-Biotech/ChemLib
Subject:	RE: Rush sequence search 09/886942

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From:	Sullivan, Daniel
Sent:	Wednesday, February 01, 2006 7:13 AM
To:	Chan, Christina
Subject:	Rush sequence search 09/886942

Hi Chris,

Please approve the following search for an after final amended case. Thanks.

Please search for the following in the pending, issued patent and commercial databases:

A nucleic acid comprising SEQ ID NO: 8;
a nucleic acid comprising the sequence from position 1 to position 909 of SEQ ID NO: 8;
a nucleic acid comprising the sequence from position 1 to position 932 of SEQ ID NO: 21.

Thank you.

Daniel M. Sullivan
Examiner AU 1636
Remsen Bldg.
Room 2A74

Tel: (571) 272-0779

Mailbox: 2C70

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OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 11:13:43   ; Search time 233.045 Seconds
                                                     (without alignments)
                                                     7291.426 Million cell updates/sec

Title: US-09-886-942-8_COPY_1_909
Perfect score: 909
Sequence: 1 atatgagggctatatacgccga.........aacggtgcattggaacgcgg 909

Scoring table: IDENTITY NUC
                Gapop 10.0 , Gapext 1.0

Searched: 3446060 seqs, 93466629 residues

Total number of hits satisfying chosen parameters: 6892120

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	864.4	95.1	8687	11	US-11-297-317-16	Sequence 16, Appl
4	864.4	95.1	9362	11	US-11-297-317-18	Sequence 18, Appl
5	864.4	95.1	9400	11	US-11-297-317-17	Sequence 17, Appl
6	810.2	89.1	5041	11	US-11-296-119-6	Sequence 6, Appl
7	810.2	89.1	5043	11	US-11-296-119-5	Sequence 5, Appl
8	810.2	89.1	5101	11	US-11-296-119-4	Sequence 4, Appl
9	810.2	89.1	5924	11	US-11-296-119-3	Sequence 3, Appl
10	810.2	89.1	5982	11	US-11-296-119-2	Sequence 2, Appl
11	810.2	89.1	6233	11	US-11-296-119-10	Sequence 10, Appl
12	810.2	89.1	17402	11	US-11-296-119-8	Sequence 8, Appl
13	810.2	89.1	18116	11	US-11-296-119-7	Sequence 7, Appl
14	787	86.6	4207	6	US-10-947-881A-4	Sequence 4, Appli
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16	787	86.6	4210	7	US-10-947-881A-5	Sequence 5, Appli
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19	787	86.6	6255	7	US-10-947-881A-13	Sequence 13, Appl
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27	779	85.7	3893	11	US-11-009-063-39	Sequence 39, Appl
28	779	85.7	3894	11	US-11-009-063-1	Sequence 1, Appl
29	779	85.7	3894	11	US-11-009-063-37	Sequence 37, Appl
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32	734	80.7	6630	11	US-11-238-171-51	Sequence 51, Appl
33	732.2	80.6	7354	9	US-11-327-232-1	Sequence 1, Appl
34	728.8	80.2	8908	11	US-11-204-755-12	Sequence 12, Appl
35	712.8	78.4	750	5	US-09-965-697A-3	Sequence 3, Appli
36	690.4	76.0	7006	11	US-11-295-006-1	Sequence 1, Appli
37	678.6	74.7	2947	11	US-11-009-063-2	Sequence 2, Appli
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39	674.4	74.2	684	1	PCT-US05-42058-69	Sequence 69, Appl
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45	660.6	72.7	10086	6	US-10-554-181-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
PCT-US05-42058-60
Sequence 60, Application PC/TUS0542058
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Kyrkanides, Stephanos
; APPLICANT: O'Banion, M. Kerry
; TITLE OF INVENTION: INFLAMMATION MODELS IN NEURODEGENERATIVE
; TITLE OF INVENTION: AND ARTHRITIC DISORDERS
; FILE REFERENCE: 21108.0046P1
; CURRENT APPLICATION NUMBER: PCT/US05/42058
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: 60/646,097
; PRIOR FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/627,604
; PRIOR FILING DATE: 2004-11-12
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 1848
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: synthetic construct
PCT-US05-42058-60

Query Match   98.1%; Score 891.4; DB 1; Length 1848;
Best Local Similarity   98.8%;
Matches 898; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy   61 ACTCTATACATTGAATCAATATTGGCCATTAAGGCCATATTATTATTGGTTATTAATAGCATAA 120
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Db 393 ACTCTATACATTGAATCAATATTGGCCATTAAGGCCATATTATTATTGGTTATTAATAGCATAA 452

Qy 121 ATCAAATAATTGGCTTATTGCCATTGCATACGTTGTATCCGTATCATAATATATGTATCATTTAT 180
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Db 453 ATCAAATAATTGGCTTATTGCCATTGCATACGTTGTATCTCATAATATATGTATCATTTAT 512

Qy 181 ATTGGCCCATGTCCAATATGACCGCCATGTTGACATTGATTAATTGACTAGTTATTAATAG 240

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OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 11:01:54 ; Search time 5767.16 seconds
(without alignments)
8714.867 Million cell updates/sec

Title: US-09-886-942-8_COPY_1_909
Perfect score: 909
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Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	909	100.0	1767	34	US-09-886-942-8	Sequence 8, Appli
2	909	100.0	3879	51	US-10-446-629-2	Sequence 2, Appli
3	909	100.0	4790	51	US-10-446-629-3	Sequence 3, Appli
4	899.4	98.9	1767	34	US-09-886-942-21	Sequence 21, Appl
5	899.4	98.9	218802	62	US-10-897-508-1	Sequence 1, Appli
6	899.4	98.9	233076	61	US-10-756-114-1	Sequence 1, Appli
7	899.4	98.9	233076	61	US-10-757-349-1	Sequence 1, Appli
8	897.8	98.8	6408	39	US-09-996-128A-1	Sequence 1, Appli
9	897.8	98.8	6485	39	US-09-996-128A-2	Sequence 2, Appli
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12	893	98.2	1767	34	US-09-886-942-16	Sequence 16, Appl
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22	891.4	98.1	7073	49	US-08-313-392-15	Sequence 15, Appl
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.7
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Run on: February 4, 2006, 11:01:54 ; Search time 11210.8 Seconds
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Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Maximum DB seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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7 c	1741.4	98.6	233076	61	US-10-757-349-1	Sequence 1, Appli
8	1737.8	98.3	6408	39	US-09-996-128A-1	Sequence 1, Appli
9	1737.8	98.3	6485	39	US-09-996-128A-2	Sequence 2, Appli
10	1728.6	97.8	1767	34	US-09-886-942-15	Sequence 15, Appli
11	1728.6	97.8	1767	34	US-09-886-942-16	Sequence 16, Appli
12	1727	97.7	1767	34	US-09-886-942-14	Sequence 14, Appl
13	1725.4	97.6	1767	34	US-09-886-942-18	Sequence 18, Appl
14 c	1720.6	97.4	1765	34	US-09-886-942-13	Sequence 13, Appl
15 c	1714.2	97.0	1767	34	US-10-521-768-2	Sequence 2, Appl
16 c	1699.8	96.2	235671	61	US-10-757-349-2	Sequence 2, Appli
17 c	1699.8	96.2	235671	61	US-10-756-114-2	Sequence 2, Appli
18	1699.8	96.2	1766	34	US-09-886-942-6	Sequence 6, Appli
19	1698.8	96.1	8251	52	US-10-521-768-4	Sequence 4, Appli
20 c	1695.2	95.9	13254	40	US-10-016-986-170	Sequence 170, App
21 c	1695.2	95.9	13254	40	US-10-016-986-156	Sequence 156, App
22	1695.2	95.9	13535	52	US-10-521-768-4	Sequence 4, Appli
23	1693.6	95.8	7073	14	US-08-480-120-15	Sequence 15, App

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(without alignments)
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Perfect score: 1767
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Scoring table: IDENTITY_NUC
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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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6	1411.8	79.9	9287	11	US-11-301-309-20	Sequence 20, Appl
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11	864.4	48.9	9400	11	US-11-297-317-18	Sequence 18, Appl
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18	810.2	45.9	17402	11	US-11-296-119-8	Sequence 8, Appl
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41	666	37.7	6783	11	US-11-274-344-14	Sequence 14, Appl
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Sequence 3, Application US/11009063
; GENERAL INFORMATION:
; APPLICANT: Robinson, Harriet L.
; APPLICANT: Amara, Rama
; APPLICANT: Ross, Ted M.
; APPLICANT: Bright, Rick A.
; TITLE OF INVENTION: DNA EXPRESSION VECTORS AND METHODS OF USE
; FILE REFERENCE: 12804-005003
; CURRENT APPLICATION NUMBER: US/11/009,063
; CURRENT FILING DATE: 2004-12-09
; PRIOR APPLICATION NUMBER: US 60/186,364
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/251,083
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/798,675
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 46
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; NAME/KEY: promoter
; LOCATION: (1)..(690)
; OTHER INFORMATION: cytomegalovirus intermediate early promoter
US-11-009-063-3

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                         GenCore version 5.1.7
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.
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16 c	1695.2	95.9	13254	6	US-10-016-986-170	Sequence 170, App
17	1692.8	95.8	2170	6	US-09-977-066-4	Sequence 4, Appli
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25	1620.4	91.7	6845	5	US-10-239-804-6	Sequence 9, Appli
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28	1619	91.6	3893	3	US-09-886-942-21	Sequence 21, Appl
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; Patent No. US2002008170BA1
; GENERAL INFORMATION:
;   APPLICANT: PUNNONEN, JUHA
;   APPLICANT: WRIGHT, ANNE
;   APPLICANT: SEMYONOV, ANDREY
; TITLE OF INVENTION: NOVEL CHIMERIC PROMOTERS
; FILE REFERENCE: 02-0319100S
; CURRENT APPLICATION NUMBER: US/09/886,942
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/213,829
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 40
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; SEQ ID NO 8
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-886-942-8

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OM nucleic - nucleic search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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Listing first 45 summaries

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SUMMARIES

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	3	1767	100.0	4790	13	ADS20070	Ads20070 pMV10.1-C
	4	1741.4	98.6	1767	6	AAL38393	Aal38393 Consensus
c	5	1741.4	98.6	218802	14	ADW98820	Adw98820 Human her
	6	1737.8	98.3	6408	8	ABX10643	Abx10643 Vector, h
	7	1737.8	98.3	6485	8	ABX10644	Abx10644 Vector, h
	8	1728.6	97.8	1767	6	AAL38377	Aal38377 Chimeric
	9	1728.6	97.8	1767	6	AAL38387	Aal38387 Chimeric
	10	1727	97.7	1767	6	AAL38388	Aal38388 Chimeric
	11	1725.4	97.6	1767	6	AAL38386	Aal38386 Chimeric
	12	1720.6	97.4	1767	6	AAL38390	Aal38390 Chimeric
	13	1720.6	97.4	1767	6	AAL38373	Aal38373 Chimeric
	14	1714.2	97.0	1765	6	AAL38385	Aal38385 Chimeric
	15	1698.8	96.1	1766	6	AAL38378	Aal38378 Chimeric
	16	1695.2	95.9	8251	12	ADJ57065	Adj57065 Vector pl
	17	1695.2	95.9	9831	14	AEB86488	Aeb86488 LAP vecto
	18	1695.2	95.9	11795	3	AAS9345	Aas9345 Nucleotid
	19	1695.2	95.9	13254	2	AAT40915	Aat40915 Nucleotid
c	20	1695.2	95.9	13254	3	AAA32151	Aaa32151 pEe12 Com
c	21	1695.2	95.9	13254	3	AAA32165	Aaa32165 Complete
c	22	1695.2	95.9	13254	3	AAA31039	Aaa31039 Complete
	23	1695.2	95.9	13535	12	ADJ57067	Adj57067 Vector pl
c	24	1695.2	95.9	229354	1	ABQ74179	Abq74179 Human cyt
	25	1694.8	95.9	2133	1	AAN91042	Aan91042 Promoter-
	26	1693.6	95.8	7073	2	AAT50962	Aat50962 TF8-5G9 C
	27	1692.8	95.8	2170	8	AAD38152	Aad38152 Human cyt
	28	1692.8	95.8	2361	8	ADA50595	Ada50595 HCMV imme
	29	1692.8	95.8	2361	14	ADW07232	Adw07232 DNA seque
	30	1692	95.8	7864	2	AAT50963	Aat50963 TF8-5G9 C
	31	1691.2	95.7	1765	6	AAL38392	Aal38392 Wild-type
	32	1688.8	95.6	13254	3	AAA31025	Aaa31025 pEe12 Com
	33	1681.6	95.2	1767	6	AAL38391	Aal38391 Wild-type
	34	1669.8	94.5	1757	6	AAL38389	Aal38389 Chimeric
	35	1665	94.2	1757	6	AAL38383	Aal38383 Chimeric
	36	1660.6	94.0	1758	6	AAL38374	Aal38374 Chimeric
	37	1621.4	91.8	8911	12	ADN07735	Adn07735 Expressio
	38	1620.6	91.7	4326	4	AAD04044	Aad04044 pWRG7077
	39	1620.6	91.7	13464	12	ADK15560	Adk15560 Hantaan/A
	40	1620.4	91.7	6845	6	ABK37491	Abk37491 Vesicular
	41	1617.4	91.5	4282	4	AAF83668	Aaf83668 pCMV-II n
	42	1617.4	91.5	7807	12	ADK15558	Adk15558 Hantaan h
	43	1617.4	91.5	7913	12	ADK15559	Adk15559 Andes han
	44	1616.4	91.5	3894	6	AAS19256	Aas19256 DNA vacci
	45	1611.4	91.2	1715	6	AAL38379	Aal38379 Chimeric

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
AAL38380

ID AAL38380 standard; DNA; 1767 BP.
XX
AC AAL38380;
XX
DT 29-AUG-2003 (revised)
DT 15-AUG-2002 (first entry)
XX
DE Chimeric sequence 6A8 from CMV promoters of human AD169/Towne strains.
XX
KW Immunomodulator; cytostatic; antibacterial; immunogenic; vaccination;
KW gene therapy; autoimmune disorder; tumour; chimeric; human; CMV promoter;
KW ds.
XX
OS Homo sapiens.
OS Chimeric.
XX
PN WO200208897-A2.
XX
PD 03-JAN-2002.
XX
PF 21-JUN-2001; 2001WO-US020123.
XX
PR 23-JUN-2000; 2000US-0213829P.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Punnonen J, Wright A, Semyonov A;
XX
DR WPI; 2002-188381/24.
XX
PT New isolated or recombinant promoter/enhancers, useful in producing a
PT prophylactic or therapeutic effect in humans, especially useful in gene
PT therapy for treating or preventing infectious diseases, autoimmune
PT disorders or tumors.
XX
PS Claim 1; Fig 8; 110pp; English.
XX
CC The invention relates to isolated or recombinant nucleic acids, which
CC comprise any of 18 sequences fully defined in the specification. The
CC nucleic acids are designated 10B2, 11B2, 12C9, 12E1, 12H9, 3C9, 4B5, 6A8,

OM nucleic - nucleic search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on: February 4, 2006, 09:23:32 ; Search time 9389.39 Seconds
(without alignments)
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Total number of hits satisfying chosen parameters: 11766282

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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	3	1741.4	98.6	1767	13	AX402409	AX402409 Sequence
	4	1741.4	98.6	1767	13	AY446869	AY446869 Human her
c	5	1741.4	98.6	25530	13	AC146851	AC146851 Human Her
c	6	1741.4	98.6	229483	13	AY315197	AY315197 Human her
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	8	1728.6	97.8	1767	6	AX402403	AX402403 Sequence
	9	1727	97.7	1767	6	AX402404	AX402404 Sequence
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	11	1720.6	97.4	1767	6	AX402406	AX402406 Sequence
	12	1714.2	97.0	1767	6	AX402401	AX402401 Sequence
	13	1704.6	96.5	229209	13	AC146907	AC146907 Human Her
c	14	1699.8	96.2	25556	13	AY446871	AY446871 Human her
c	15	1699.8	96.2	226889	13	AC146905	AC146905 Human Her
	16	1698.0	96.1	1766	6	AX402394	AX402394 Sequence
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c	18	1695.2	95.9	2133	6	A01323	A01323 Human cytom
c	19	1695.2	95.9	11795	6	AX027785	AX027785 Sequence
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c	21	1695.2	95.9	13254	6	AR038321	AR038321 Sequence
c	22	1695.2	95.9	13254	6	I58610	I58610 Sequence 17
c	23	1695.2	95.9	13254	6	I58596	I58596 Sequence 15
c	24	1695.2	95.9	229354	6	AR474465	AR474465 Sequence
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c	26	1695.2	95.9	229354	6	AX686187	AX686187 Sequence
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c	29	1692.8	95.8	2170	6	AR656224	AR656224 Sequence
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c	31	1692.8	95.8	2361	13	HSMIEP	HSMIEP Human cytom
c	32	1681.6	95.2	1767	6	AX402407	AX402407 Sequence
c	33	1679.2	95.0	25572	13	AY446866	AY446866 Human her
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c	35	1672.6	94.7	24589	13	AY446870	AY446870 Human her
c	36	1671.2	94.6	234881	13	AC146906	AC146906 Human Her
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c	39	1665	94.2	1757	6	AX402399	AX402399 Sequence
c	40	1665	94.2	25616	13	AY446864	AY446864 Human her
c	41	1662.6	94.1	1758	6	AY446894	AY446894 Human her
c	42	1638.4	92.7	235645	13	AX402390	AX402390 Sequence
c	43	1636	92.6	25770	13	AY446868	AY446868 Human her
c	44	1625	92.0	25489	13	AY446867	AY446867 Human her
c	45	1625	92.0	229700	13	AC146904	AC146904 Human Her

ALIGNMENTS

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AX402396

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LOCUS       AX402396                1767 bp    DNA     linear   PAT 07-JUN-2002
DEFINITION  Sequence 8 from Patent WO0200897.
ACCESSION   AX402396
VERSION     AX402396.1  GI:21387431
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Punnonen,J., Wright,A. and Semyonov,A.
  TITLE     Novel chimeric promoters
  JOURNAL   Patent: WO 0200897-A 8 03-JAN-2002;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
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                     /note="Synthetic oligonucleotide"

ORIGIN

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  Best Local Similarity   100.0%;
  Matches 1767;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 ATATGAGGCTATATCGCCGATAGAGGCGACATCAAGCCGGCACATGGCCAATGCATATCG 60

Qy         61 ATCTATACATTGAATCAATATATGGGTTATATGGCAATTAGCCATATTAGGCAATTAGGCGCATA 120
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Db         61 ATCTATACATTGAATCAATATATGGGTTATATGGCAATTAGCCATATTAGGCAATTAGGCGCATAA 120

Qy        121 ATCAATATTGGCTATTGGCCATTGACTACACGTTGATCCGTATCCGTATCATAATATGTTGACATTAT 180
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Qy        181 ATTGGGCCCATGTCCAAATATGACCGCCATGTTGACATTGAATTATTGACTAGTTATTAATAG 240
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.7

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Perfect score: 1767
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Scoring table: IDENTITY NUC
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1695.2	95.9	8251	7	US-10-521-768-2	Sequence 2, Appli
2	1695.2	95.9	13535	7	US-10-521-768-4	Sequence 4, Appli
3	1603.6	90.8	7003	8	US-11-193-750-1	Sequence 1, Appli
4	1603.6	90.8	7073	8	US-11-038-933-2	Sequence 2, Appli
5	1603.6	90.8	7272	8	US-11-038-933-4	Sequence 4, Appli
6	1603.6	90.8	7285	8	US-11-038-933-3	Sequence 3, Appli
7	1585.8	89.7	5302	7	US-10-401-386B-81	Sequence 81, Appli
8	1579	89.4	5089	8	US-11-179-798-2	Sequence 2, Appli
9	1579	89.4	5089	8	US-11-179-798-5	Sequence 5, Appli
10	1579	89.4	5488	8	US-11-179-799-3	Sequence 3, Appli
11	1579	89.4	5488	8	US-11-179-798-6	Sequence 6, Appli
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13	1579	89.4	5500	8	US-11-179-798-4	Sequence 4, Appli
14	1576.4	89.2	10369	7	US-10-521-768-3	Sequence 3, Appli
15	1574.4	89.1	3547	8	US-11-115-425-100	Sequence 100, App
16	1572.8	89.0	4432	8	US-11-115-425-14	Sequence 14, Appl
17	1572.8	89.0	4864	8	US-11-115-425-12	Sequence 12, Appl
18	1572.4	89.0	2196	8	US-11-115-425-13	Sequence 13, Appl
19	1565.2	88.6	6245	7	US-10-401-386B-61	Sequence 61, Appl
20	1521.8	86.1	12745	6	US-10-978-927-8	Sequence 8, Appl
21	1368.6	77.5	1848	6	US-10-978-927-32	Sequence 32, Appl
22	810.2	45.9	5041	8	US-11-193-750-6	Sequence 6, Appl
23	810.2	45.9	5043	8	US-11-193-750-5	Sequence 5, Appl
24	810.2	45.9	5101	8	US-11-193-750-4	Sequence 4, Appli
25	810.2	45.9	5924	8	US-11-193-750-3	Sequence 3, Appli
26	810.2	45.9	5982	8	US-11-193-750-2	Sequence 2, Appli
27	810.2	45.9	6233	8	US-11-193-750-10	Sequence 10, Appli
28	810.2	45.9	17402	8	US-11-193-750-8	Sequence 8, Appli
29	810.2	45.9	18116	8	US-11-193-750-7	Sequence 7, Appli
30	751.2	42.5	6741	6	US-10-813-646-21	Sequence 21, Appli
31	749.4	42.4	4775	7	US-10-401-386B-62	Sequence 62, Appli
32	748.8	42.4	3913	6	US-10-981-267-27	Sequence 27, Appli
33	748.2	42.3	5391	6	US-10-981-356A-44	Sequence 44, Appli
34	748.2	42.3	5391	8	US-11-106-046-44	Sequence 44, Appl
35	748.2	42.3	5988	8	US-11-106-820-21	Sequence 21, Appl
36	748.2	42.3	6135	8	US-11-159-919-17	Sequence 17, Appl
37	748.2	42.3	6135	6	US-10-981-356A-45	Sequence 45, Appl
38	748.2	42.3	6135	8	US-11-096-046-45	Sequence 45, Appl
39	748.2	42.3	7496	8	US-11-106-820-22	Sequence 22, Appl
40	748.2	42.3	7127	8	US-11-192-219-46	Sequence 46, Appl
41	748.2	42.3	7201	8	US-11-159-919-16	Sequence 16, Appl
42	748.2	42.3	7094	8	US-11-159-919-15	Sequence 15, Appl
43	736.4	41.7	33014	8	US-11-077-716-1	Sequence 1, Appli
44	734.8	41.6	9117	8	US-11-003-967-26	Sequence 26, Appl
45	734	41.5	6630	8	US-11-065-716-51	Sequence 51, Appl

ALIGNMENTS

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US-10-521-768-2
Sequence 2, Application US/10521768
Publication No. US20060003405A1
GENERAL INFORMATION:
; APPLICANT: Lonza Biologics plc.
; TITLE OF INVENTION: Method of expressing recombinant protein in CHO cells
; FILE REFERENCE: 4145-22
; CURRENT APPLICATION NUMBER: US/10/521,768
; CURRENT FILING DATE: 2005-01-19
; PRIOR APPLICATION NUMBER: PCT/EP2003/007946
; PRIOR FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: GB 0216648.6
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 8251
;   TYPE: DNA
;   ORGANISM: Hamster sp.
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Seq. ID. No .3: circular plasmid GS vector p12.4 hCMVp-GFP /clon
; US-10-521-768-2

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Db   5921 ATTGGGCTCATGTCCAACATTACCGCCATGTTGACATTGACTAGTTATTAATAG 5980

OM nucleic - nucleic search, using sw model

GenCore version 5.1.7
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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3	1695.2	95.9	13254	2	US-08-899-575-156	Sequence 156, App
4	1695.2	95.9	13254	2	US-08-899-575-170	Sequence 170, App
5	1695.2	95.9	13254	2	US-08-899-575-156	Sequence 156, App
6	1695.2	95.9	13254	2	US-08-899-575-170	Sequence 170, App
7	1695.2	95.9	13254	6	PCT-US95-08743-156	Sequence 156, App
8	1695.2	95.9	13254	6	PCT-US95-08743-170	Sequence 170, App
9	1695.2	95.9	229354	3	US-09-705-400-64	Sequence 64, Appl
10	1692.8	95.8	2170	3	US-09-977-066A-4	Sequence 4, Appl
11	1620.6	91.7	4326	3	US-08-760-615-7	Sequence 7, Appl
12	1603.6	90.8	5108	3	US-09-628-730-51	Sequence 51, Appl
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17	1603.6	90.8	5254	3	US-09-628-730-60	Sequence 60, Appl
18	1603.6	90.8	7003	3	US-09-913-909-1	Sequence 1, Appli
19	1603.6	90.8	7073	3	US-09-913-909-2	Sequence 2, Appli
20	1603.6	90.8	7272	3	US-09-913-909-4	Sequence 4, Appli
21	1603.6	90.8	7285	3	US-09-913-909-3	Sequence 3, Appli
22	1590.6	90.0	15538	3	US-09-554-337-1	Sequence 1, Appli
23	1581	89.5	4928	2	US-08-345-913-1	Sequence 1, Appli
24	1581	89.5	4928	3	US-08-818-562-1	Sequence 1, Appli
25	1581	89.5	4928	3	US-09-628-445-1	Sequence 1, Appli
26	1574.4	89.1	3547	3	US-09-340-798A-43	Sequence 43, Appl
27	1574.4	89.1	3610	3	US-09-194-949A-1	Sequence 1, Appli
28	1574.4	89.1	4261	3	US-09-194-949A-25	Sequence 25, Appl
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ALIGNMENTS

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Sequence 156, Application US/08276852
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; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 156:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13254 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 09:23:32 ; Search time 4830.2 Seconds
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	899.4	98.9	231236	13	AY315197	AY315197 Human her
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17	891.4	98.1	13254	6	I58596	I58596 Sequence 15
18	891.4	98.1	13254	6	I58610	I58610 Sequence 17
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37	874.8	96.2	2170	6	AR656224	AR656224 Sequence
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ALIGNMENTS

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VERSION   AX402396.1 GI:21387431
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SOURCE   synthetic construct
  ORGANISM synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Punnonen,J., Wright,A. and Semyonov,A.
  TITLE   Novel chimeric promoters
  JOURNAL   Patent: WO 0200897-A 8 03-JAN-2002;
            Maxygen, Inc. (US)
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ORIGIN

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Qy   181 ATTGGCCCANGTCCAATATGACCCGCCATGTTGACATTGATTATTGAGTAGTTATTAATAG 240
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.7
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Run on: February 4, 2006, 09:16:57 ; Search time 601.381 Seconds
(without alignments)
10073.821 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	909	100.0	4790	13	ADS20070	Ads20070 pMV10.1-C
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10	893	98.2	1767	6	AAL38387	Aal38387 Chimeric
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13	891.4	98.1	2133	6	AAN91042	Aan91042 Promoter-
14	891.4	98.1	6845	6	ABK37491	Abk37491 Vesicular
15	891.4	98.1	7073	2	AAT50962	Aat50962 TF8-5G9 C
16	891.4	98.1	7864	2	AAT50963	Aat50963 TF8-5G9 C
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22	891.4	98.1	13254	3	AAA32165	Aaa32165 Complete
23	891.4	98.1	13254	3	AAA31039	Aaa31039 Complete
24	891.1	98.1	13535	12	ADJ57067	Adj57067 Vector pl
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29	885.8	97.4	1765	6	AAL38385	Aal38385 Chimeric
30	885	97.4	1767	6	AAL38390	Aal38390 Chimeric
31	883.6	97.2	1766	6	AAL38378	Aal38378 Chimeric
32	879.4	96.7	1767	6	AAL38391	Aal38391 Wild-type
33	874.8	96.2	912	2	AAZ09519	Aaz09519 Human CMV
34	874.8	96.2	1765	6	AAL38392	Aal38392 Wild-type
35	874.8	96.2	2170	6	AAD38152	Aad38152 Human cyt
36	874.8	96.2	2361	8	ADA50595	Ada50595 HCMV imme
37	874.8	96.2	2361	14	ADW07232	Adw07232 DNA seque
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39	867.4	95.4	8135	2	AAQ90134	Aaq90134 Plasmid p
40	867.4	95.4	8135	2	AAQ90136	Aaq90136 Plasmid p
41	867.4	95.4	8149	2	AAQ90133	Aaq90133 Plasmid p
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45	864.4	95.1	8687	14	ADY80264	Ady80264 Nucleotid

ALIGNMENTS

RESULT 1
AAL38380

ID   AAL38380 standard; DNA; 1767 BP.
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AC   AAL38380;
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DT   15-AUG-2002 (first entry)
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DE   Chimeric sequence 6A8 from CMV promoters of human AD169/Towne strains.
XX
KW   Immunomodulator; cytostatic; antibacterial; immunogenic; vaccination;
KW   gene therapy; autoimmune disorder; tumour; chimeric; human; CMV promoter;
KW   ds.
XX
OS   Homo sapiens.
OS   Chimeric.
XX
PN   WO20020200897-A2.
XX
PD   03-JAN-2002.
XX
PF   21-JUN-2001; 2001WO-US020123.
XX
PR   23-JUN-2000; 2000US-0213829P.
XX
PA   (MAXY-) MAXYGEN INC.
PI   Punnonen J, Wright A, Semyonov A;
XX
DR   WPI; 2002-188381/24.
XX
PT   New isolated or recombinant promoter/enhancers, useful in producing a
PT   prophylactic or therapeutic effect in humans, especially useful in gene
PT   therapy for treating or preventing infectious diseases, autoimmune
PT   disorders or tumors.
PS   Claim 1; Fig 8; 110pp; English.
XX
CC   The invention relates to isolated or recombinant nucleic acids, which
CC   comprise any of 18 sequences fully defined in the specification. The
CC   nucleic acids are designated 10B2, 11E2, 12C9, 12E1, 12H9, 3C9, 4B5, 6A8,

OM nucleic - nucleic search, using sw model

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                    GenCore version 5.1.7
                    Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on:             February  4, 2006, 15:25:23 ; Search time 220.951 Seconds
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SUMMARIES

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5	810.2	89.1	5043	8	US-11-193-750-5	Sequence 5, Appli
6	810.2	89.1	5101	8	US-11-193-750-4	Sequence 4, Appli
7	810.2	89.1	5924	8	US-11-193-750-3	Sequence 3, Appli
8	810.2	89.1	5982	8	US-11-193-750-2	Sequence 2, Appli
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11	810.2	89.1	18116	8	US-11-193-750-7	Sequence 7, Appl
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26	763	83.9	5500	8	US-11-179-798-1	Sequence 1, Appli
27	763	83.9	5500	8	US-11-179-798-4	Sequence 4, Appli
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34	708	77.9	12745	6	US-10-981-356A-44	Sequence 44, Appl
35	690	75.9	5391	6	US-10-981-356A-45	Sequence 45, Appl
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38	690	75.9	5988	8	US-11-159-919-17	Sequence 17, Appl
39	690	75.9	6135	6	US-10-981-356A-45	Sequence 45, Appl
40	690	75.9	6135	8	US-11-096-046-45	Sequence 45, Appl
41	690	75.9	6135	8	US-11-106-820-22	Sequence 22, Appl
42	690	75.9	6741	6	US-10-813-646-21	Sequence 21, Appl
43	690	75.9	7127	8	US-11-192-219-46	Sequence 46, Appl
44	690	75.9	7201	8	US-11-159-919-16	Sequence 16, Appl
45	690	75.9	7496	8	US-11-159-919-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-10-978-927-32
; Sequence 32, Application US/10978927
; Publication No. US20060009406A1
; GENERAL INFORMATION:
; APPLICANT: Kyrkanides, Stephanos
; TITLE OF INVENTION: VECTORS HAVING BOTH ISOFORMS OF
; TITLE OF INVENTION: BETA-HEXOSAMINIDASE
; FILE REFERENCE: 21108.0018U2
; CURRENT APPLICATION NUMBER: US/10/978,927
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: PCT/US03/13672
; PRIOR APPLICATION NUMBER: 60/377,503
; PRIOR FILING DATE: 2003-05-02
; PRIOR FILING DATE: 2002-05-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 1848
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./Note =
; OTHER INFORMATION: Synthetic Construct
US-10-978-927-32

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Best Local Similarity 98.8%;   Pred. No. 1.7e-265;
Matches 898; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy        121 ATCAATATTGGCTATTGGCCATTGCATACGTTGTATCCGTATCATAATAGTACATTAT 180
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 13:11:03 ; Search time 1069,74 Seconds
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Perfect score: 909
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Scoring table: IDENTITY_NUC
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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	909	100.0	1767	3	US-09-886-942-8	Sequence 8, Appli
2	909	100.0	3879	7	US-10-446-629-2	Sequence 2, Appli
3	909	100.0	4790	7	US-10-446-629-3	Sequence 3, Appli
4	899.4	98.9	1767	3	US-09-886-942-21	Sequence 21, Appl
5	899.4	98.9	218802	9	US-10-097-508-1	Sequence 1, Appli
6	897.8	98.8	6408	3	US-09-996-128A-1	Sequence 1, Appli
7	897.8	98.8	6485	3	US-09-996-128A-2	Sequence 2, Appli
8	893	98.2	1767	3	US-09-886-942-5	Sequence 5, Appli
9	893	98.2	1767	3	US-09-886-942-15	Sequence 15, Appli
10	893	98.2	1848	3	US-10-781-142-32	Sequence 32, Appl
11	891.4	98.1	1767	3	US-09-886-942-16	Sequence 16, Appl
12	891.4	98.1	6845	5	US-10-239-804-6	Sequence 6, Appl
13	891.4	98.1	6845	8	US-10-838-906-26	Sequence 26, Appl
14	891.4	98.1	13254	6	US-10-016-986-156	Sequence 156, App
15	891.4	98.1	13254	6	US-10-016-986-170	Sequence 170, App
16	889.8	97.9	1767	3	US-09-886-942-14	Sequence 14, Appl
17	885.8	97.4	1765	3	US-09-886-942-13	Sequence 13, Appl
18	885	97.4	1767	3	US-09-886-942-18	Sequence 18, Appl
19	883.6	97.2	1766	3	US-09-886-942-6	Sequence 6, Appli
20	879.4	96.7	1767	3	US-09-886-942-19	Sequence 19, Appl
21	874.8	96.2	912	6	US-10-223-507-52	Sequence 52, Appl
22	874.8	96.2	1665	3	US-09-886-942-20	Sequence 20, Appl
23	874.8	96.2	2170	3	US-09-977-066-4	Sequence 4, Appli
24	874.8	96.2	2170	10	US-11-103-805-4	Sequence 4, Appli
25	864.4	95.1	8687	7	US-10-467-546-15	Sequence 15, Appli
26	864.4	95.1	8687	7	US-10-467-546-16	Sequence 16, Appli
27	864.4	95.1	8687	9	US-10-666-332-15	Sequence 15, Appli
28	864.4	95.1	8687	9	US-10-666-332-16	Sequence 16, Appl
29	864.4	95.1	9362	7	US-10-467-546-18	Sequence 18, Appl
30	864.4	95.1	9362	9	US-10-666-332-18	Sequence 18, Appl
31	864.4	95.1	9400	9	US-10-467-546-17	Sequence 17, Appl
32	864.4	95.1	9400	9	US-10-666-332-17	Sequence 17, Appl
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34	858.4	94.4	3570	10	US-11-881-457A-1	Sequence 1, Appli
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36	831.4	91.5	1757	3	US-09-886-942-2	Sequence 2, Appl
37	831	91.4	1758	9	US-10-666-332-11	Sequence 11, Appl
38	827.4	91.0	897	3	US-09-886-942-3	Sequence 3, Appli
39	821	90.3	897	9	US-10-206-747-2	Sequence 2, Appli
40	821	90.3	930	5	US-10-206-747-4	Sequence 4, Appli
41	810.2	89.1	930	9	US-09-886-942-9	Sequence 9, Appli
42	810.2	89.1	5041	8	US-10-790-455-6	Sequence 6, Appl
43	810.2	89.1	5041	8	US-10-811-136B-6	Sequence 6, Appl
44	810.2	89.1	5041	9	US-10-940-315-6	Sequence 6, Appl
45	810.2	89.1	5041	10	US-11-068-155-6	Sequence 6, Appli

ALIGNMENTS

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US-09-886-942-8
; Sequence 8, Application US/09886942
; Patent No. US2002000181708A1
; GENERAL INFORMATION:
;   APPLICANT: PUNNONEN, JUHA
;   APPLICANT: WRIGHT, ANNE
;   APPLICANT: SEMYONOV, ANDREY
;   TITLE OF INVENTION: NOVEL CHIMERIC PROMOTERS
;   FILE REFERENCE: 02-0319100S
;   CURRENT APPLICATION NUMBER: US/09/886,942
;   CURRENT FILING DATE: 2001-06-21
;   PRIOR APPLICATION NUMBER: 60/213,829
;   PRIOR FILING DATE: 2000-06-23
;   NUMBER OF SEQ ID NOS: 40
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 8
;   LENGTH: 1767
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-886-942-8

  Query Match   100.0%; Score 909; DB 3; Length 1767;
  Best Local Similarity   100.0%; Pred. No. 1.2e-249;
  Matches 909; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   61 ATCTATACATTGAATCAATATTGGCCATTGCATACGTTGTATCCGTATCATAATATGTACATTTAT 120
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Qy   121 ATCAATATTGGCTATTGGCCATTGCATAACGTTGTATCCGTATCATAATATGTACATTTAT 180
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Qy   181 ATTGGGCCCATGTCCAAATATGACCGGCCATGTTGACATTGATTAATTGACTAGTTATTAATTAG 240
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Db   181 ATTGGGCCCATGTCCAAATATGACCGGCCATGTTGACATTGATTAATTGACTAGTTATTAATTAG 240

GenCore version 5.1.7

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Om nucleic - nucleic search, using sw model

Run on: February 4, 2006, 10:33:48 ; Search time 176.862 Seconds
(without alignments)
9135.958 Million cell updates/sec

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Perfect score: 909

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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c	4	891.4	98.1	13254	2	US-08-899-575-170	Sequence 170, App
c	5	891.4	98.1	13254	2	US-08-899-575-156	Sequence 156, App
c	6	891.4	98.1	13254	2	US-08-899-575-170	Sequence 170, App
c	7	891.4	98.1	13254	6	PCT-US95-08743-156	Sequence 156, App
c	8	891.4	98.1	13254	6	PCT-US95-08743-170	Sequence 170, App
c	9	891.4	98.1	229354	3	US-09-705-400-64	Sequence 64, App
c	10	874.8	96.2	912	3	US-09-495-052-52	Sequence 52, App
c	11	874.8	96.2	2170	3	US-09-977-066A-4	Sequence 4, Appl
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	14	821	90.3	930	2	US-08-029-022-2	Sequence 2, Appli
	15	821	90.3	930	4	US-08-029-022-4	Sequence 4, Appli
	16	821	90.3	930	2	US-08-246-376-2	Sequence 2, Appli
	17	821	90.3	930	4	US-08-246-376-4	Sequence 4, Appli
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	20	821	90.3	930	2	US-08-256-004-2	Sequence 2, Appli
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	28	821	90.3	930	2	PCT-US93-05366-2	Sequence 2, Appli
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	30	787	86.6	4207	3	US-09-897-511A-4	Sequence 4, Appl
	31	787	86.6	4210	3	US-09-897-511A-5	Sequence 5, Appl
	32	787	86.6	6255	3	US-09-897-511A-13	Sequence 13, Appl
	33	786.4	86.5	7352	3	US-08-786-531B-4	Sequence 4, Appl
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	35	786.4	86.5	8560	3	US-09-936-572-11	Sequence 11, Appl
	36	786.4	86.5	9511	3	US-09-897-511A-34	Sequence 34, Appl
	37	786.4	86.5	11299	3	US-08-760-615-7	Sequence 7, Appl
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ALIGNMENTS

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; Sequence 156, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 13254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

OM nucleic - nucleic search, using sw model

GenCore version 5.1.7
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Run on: February 4, 2006, 09:23:32 ; Search time 4952.41 Seconds (without alignments)
10697.432 Million cell updates/sec

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Perfect score: 932
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 5883141 seqs, 2842172565653 residues
Total number of hits satisfying chosen parameters: 11766282
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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c	4	932	100.0	231236	13	AY315197	AY315197 Human her
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c	6	922.4	99.0	1767	6	AX402393	AX402393 Sequence
c	7	922.4	99.0	1767	6	AX402396	AX402396 Sequence
	8	922.4	99.0	1767	6	AX402402	AX402402 Sequence
	9	922.4	99.0	1767	11	DQ000968	DQ000968 Synthetic
	10	920.8	98.8	1767	6	AX402404	AX402404 Sequence
	11	916	98.3	1767	6	AX402406	AX402406 Sequence
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c	14	914.4	98.1	2133	6	A01323	A01323 Human cytom
c	15	914.4	98.1	6845	6	AX268212	AX268212 Sequence
	16	914.4	98.1	11795	6	AX027785	AX027785 Sequence
	17	914.4	98.1	13254	6	AR038307	AR038307 Sequence
c	18	914.4	98.1	13254	6	AR038321	AR038321 Sequence
c	19	914.4	98.1	13254	6	I58596	I58596 Sequence 15
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c	23	914.4	98.1	229354	6	AR474465	AR474465 Sequence
c	24	914.4	98.1	229354	6	AR475529	AR475529 Sequence
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c	26	914.4	98.1	229354	13	X17403	X17403 Human cytom
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c	32	907.4	97.4	2170	6	AX451705	AX451705 Sequence
c	33	907.4	97.4	2361	13	HSSMIEP	M60321 Human Her
c	34	906.4	97.3	229209	13	AC146907	AC146907 Human Her
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c	41	898.4	96.4	229700	13	AC146904	AC146904 Human her
c	42	896.8	96.2	25770	13	AY446868	AY446868 Human her
c	43	896.6	96.2	1765	6	AX402401	AX402401 Sequence
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ALIGNMENTS

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DEFINITION  Sequence 21 from Patent WO0200897.
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VERSION     AX402409.1  GI:21387444
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Punnonen,J., Wright,A. and Semyonov,A.
  TITLE     Novel chimeric promoters
  JOURNAL   Patent: WO 0200897-A 21 03-JAN-2002;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
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Best Local Similarity 100.0%;
Matches 932; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   61 ATCTATACATTGAAATCAAATATTGGCCAATTAGGCCATAATTAGTCATTGGTTATAAA 120
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Qy  121 ATCAATATTGGCTATTGGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTAT 180
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Db  181 ATTGGCTCATCTCCAATATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAG 240
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GenCore version 5.1.7
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Run on: February 4, 2006, 09:16:57 ; Search time 616.598 Seconds

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No. is the number of results satisfying chosen parameters.

SUMMARIES

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13	916	98.3	1767	6	AAL38390	Aal38390 Chimeric
14	914.4	98.1	1848	8	ADA50596	Ada50596 HCMV imme
15	914.4	98.1	2133	12	ADF53547	Adf53547 Human CMV
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17	914.4	98.1	6845	6	ABK37491	Abk37491 Vesicular
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32	907.4	97.4	2170	6	AAD38152	Aad38152 Human cyt
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ALIGNMENTS

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AC   AAL38393;
XX
DT   15-AUG-2002 (first entry)
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DE   Consensus sequence of AD169 and Towne CMV promoters.
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KW   Immunomodulator; cytostatic; antibacterial; immunogenic; vaccination;
KW   gene therapy; autoimmune disorder; tumour; CMV promoter; human;
KW   wild-type; ds.
XX
OS   Unidentified.
XX
PN   WO20020200897-A2.
XX
PD   03-JAN-2002.
XX
PF   21-JUN-2001; 2001WO-US020123.
XX
PR   23-JUN-2000; 2000US-0213829P.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Punnonen J, Wright A, Semyonov A;
XX
DR   WPI; 2002-188381/24.
XX
PT   New isolated or recombinant promoter/enhancers, useful in producing a
PT   prophylactic or therapeutic effect in humans, especially useful in gene
PT   therapy for treating or preventing infectious diseases, autoimmune
PT   disorders or tumors.
XX
PS   Disclosure; Fig 8; 110pp; English.
XX
CC   The invention relates to isolated or recombinant nucleic acids, which
CC   comprise any of 18 sequences fully defined in the specification. The
CC   nucleic acids are designated 10B2, 11E2, 12C9, 12E1, 12H9, 3C9, 4B5,
CC   6B2, 6D4, 6F6, 9E1, 9F11, 9G11, 9G12, 9G4, 9G7 and 9G8, and comprise 898-
CC   1768 base pair sequences. The nucleic acids are useful in producing an

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                          GenCore version 5.1.7
                          Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Run on:        February 4, 2006, 13:11:03 ; Search time 1096.8 Seconds
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.
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SUMMARIES

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5	925.6	99.3	1767	3	US-10-467-546-15	Sequence 15, Appl
6	922.4	99.0	1767	3	US-10-666-332-16	Sequence 16, Appl
7	922.4	99.0	1767	3	US-09-886-944-5	Sequence 5, Appl
8	922.4	99.0	1767	3	US-09-886-942-8	Sequence 8, Appl
9	922.4	99.0	1767	3	US-09-886-942-14	Sequence 14, Appl
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c 17	914.4	98.1	13254	6	US-10-016-986-156	Sequence 156, App
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22	902.4	96.8	2170	10	US-11-103-805-4	Sequence 4, Appli
23	896.6	96.2	1765	3	US-09-886-942-13	Sequence 13, Appl
24	887.4	95.2	912	6	US-10-223-507-52	Sequence 52, Appl
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29	864.4	92.7	8687	9	US-10-467-546-16	Sequence 16, Appl
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43	815	87.4	5041	8	US-10-940-315-6	Sequence 6, Appli
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ALIGNMENTS

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; Patent No. US2002008170BA1
; GENERAL INFORMATION:
;   APPLICANT: PUNNONEN, JUHA
;   APPLICANT: WRIGHT, ANNE
;   APPLICANT: SEMYONOV, ANDREY
;   APPLICANT:
;   TITLE OF INVENTION: NOVEL CHIMERIC PROMOTERS
;   FILE REFERENCE: 02-031910US
;   CURRENT APPLICATION NUMBER: US/09/886,942
;   CURRENT FILING DATE: 2001-06-21
;   PRIOR APPLICATION NUMBER: 60/213,829
;   PRIOR FILING DATE: 2000-06-23
;   NUMBER OF SEQ ID NOS: 40
;   SOFTWARE: Patentin Ver. 2.1
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;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Consensus
;   OTHER INFORMATION: sequence

US-09-886-942-21

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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.7

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Post-processing: Minimum Match 0%
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3	914.4	98.1	13555	7	US-11-038-933-2	Sequence 2, Appli
4	815	87.4	5041	8	US-10-521-768-2	Sequence 4, Appli
5	815	87.4	5043	8	US-11-193-750-6	Sequence 5, Appli
6	815	87.4	5101	8	US-11-193-750-4	Sequence 4, Appli
7	815	87.4	5524	8	US-11-193-750-3	Sequence 3, Appli
8	815	87.4	5992	8	US-11-193-750-2	Sequence 2, Appli
9	815	87.4	6233	8	US-11-193-750-10	Sequence 10, Appl
10	815	87.4	17402	8	US-11-193-750-8	Sequence 8, Appl
11	815	87.4	18816	8	US-11-193-750-7	Sequence 7, Appl
12	795.6	85.4	10369	7	US-10-521-768-3	Sequence 3, Appl
13	794	85.2	6245	7	US-11-038-933-61	Sequence 61, Appl
14	793.6	85.2	3547	8	US-11-401-386B-61	Sequence 100, App
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16	792.4	85.0	5089	8	US-11-179-798-5	Sequence 5, Appl
17	792.4	85.0	5488	8	US-11-179-798-3	Sequence 3, Appl
18	792.4	85.0	5488	8	US-11-179-798-6	Sequence 6, Appl
19	792.4	85.0	5500	8	US-11-179-798-1	Sequence 1, Appl
20	792.4	85.0	5500	8	US-11-179-798-4	Sequence 4, Appl
21	792	85.0	4432	8	US-11-115-425-12	Sequence 12, Appl
22	792	85.0	4864	8	US-11-115-425-14	Sequence 14, Appl
23	792	85.0	7003	8	US-11-038-933-1	Sequence 1, Appli
24	792	85.0	7073	8	US-11-038-933-2	Sequence 2, Appli
25	792	85.0	7272	8	US-11-038-933-4	Sequence 4, Appli
26	792	85.0	7285	8	US-11-038-933-3	Sequence 3, Appli
27	791.6	84.9	2196	8	US-11-115-425-13	Sequence 13, Appl
28	782.6	84.0	5302	7	US-10-401-386B-81	Sequence 81, Appl
29	757.4	81.3	4775	7	US-10-401-386B-62	Sequence 62, Appl
30	739.6	79.4	9117	8	US-11-003-967-26	Sequence 26, Appl
31	738.6	79.3	6630	8	US-11-065-716-51	Sequence 51, Appl
32	734.2	78.8	12745	6	US-11-978-927-8	Sequence 8, Appl
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34	719.2	77.2	4800	7	US-10-855-490C-49	Sequence 49, Appl
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38	711.4	76.3	5988	8	US-11-159-919-17	Sequence 17, Appl
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42	711.4	76.3	6741	8	US-10-813-646-21	Sequence 21, Appl
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ALIGNMENTS

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US-10-978-927-32
; Sequence 32, Application US/10978927
; Publication No. US2006009406A1
; GENERAL INFORMATION:
; APPLICANT: Kyrkanides, Stephanos
; TITLE OF INVENTION: VECTORS HAVING BOTH ISOFORMS OF
; TITLE OF INVENTION: BETA-HEXOSAMINIDASE
; FILE REFERENCE: 21108.0018U2
; CURRENT APPLICATION NUMBER: US/10/978,927
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: PCT/US03/13672
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/377,503
; PRIOR FILING DATE: 2002-05-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 1848
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-978-927-32

Query Match   98.1%;   Score 914.4;   DB 6;   Length 1848;
Best Local Similarity   98.8%;
Matches   921;   Conservative   0;   Mismatches   11;   Indels   0;   Gaps   0;

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Qy      1 ATATGAGGCTATATCGCCCGATAGAGGCGACATCAAGCTGGCACATGGCCAAATGCATATCG 60
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Db    333 ATATGAGGCTATATCGCCCGATAGAGGCGACATCAAGCTGGCACATGGCCAAATGCATATCG 392

Qy     61 ATCTATACATTGAATCAATATTGGCAATATTAGTCATTGGTTATTATATAGGCATAA 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    393 ATCTATACATTGAATCAATATTGGCCATTAGCCATATTATTCATTGGTTATTATATAGGCATAA 452

Qy    121 ATCAATATATTGGCTATTGTCGATTACGTTGTATCTATATCATAATAATGTACATTTAT 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    453 ATCAATATATTGGCTATTGTCGATTACGTTGTATCCATATCATAATAATGTACATTTAT 512

Qy    181 ATTGGCTCATGTCCAATATGACCCCCATGTTGACATTGATTATTGACTAGTTATTAATAG 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    513 ATTGGCTCATGTCCAACATTACCGCCCATGTTGACATTGATTATTGACTAGTTATTAATAG 572
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.7

Run on: February 4, 2006, 10:33:48 ; Search time 181.337 Seconds
                                              (without alignments)
                                              9135.958 Million cell updates/sec

Title: US-09-886-942-21_COPY_1_932
Perfect score: 932
Sequence: 1 atatgaggctatatcgccga...........cccgtgccaagagtgacgt 932

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
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    2: /cgn2_6/ptcdata/1/ina/5_COMB.seq:*
    3: /cgn2_6/ptcdata/1/ina/6A_COMB.seq:*
    4: /cgn2_6/ptcdata/1/ina/6B_COMB.seq:*
    5: /cgn2_6/ptcdata/1/ina/H_COMB.seq:*
    6: /cgn2_6/ptcdata/1/ina/PCTUS_COMB.seq:*
    7: /cgn2_6/ptcdata/1/ina/PP_COMB.seq:*
    8: /cgn2_6/ptcdata/1/ina/RE_COMB.seq:*
    9: /cgn2_6/ptcdata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	* Query Match Length	DB	ID	Description
1	914.4	98.1	13254	2	US-08-276-852-156	Sequence 156, App
2	914.4	98.1	13254	2	US-08-276-852-170	Sequence 170, App
3	914.4	98.1	13254	2	US-08-899-575-156	Sequence 156, App
4	914.4	98.1	13254	2	US-08-899-575-170	Sequence 170, App
5	914.4	98.1	13254	2	US-08-899-575-156	Sequence 156, App
6	914.4	98.1	13254	2	US-08-899-575-170	Sequence 170, App
7	914.4	98.1	13254	6	PCT-US95-08743-156	Sequence 156, App
8	914.4	98.1	13254	6	PCT-US95-08743-170	Sequence 170, App
9	914.4	98.1	229354	3	US-09-705-400-64	Sequence 64, Appl
10	907.4	97.4	2170	3	US-09-977-066A-4	Sequence 4, Appl
11	887.4	95.2	912	3	US-09-495-052-52	Sequence 52, Appl
12	868	93.1	3570	3	US-09-881-457A-1	Sequence 1, Appl
13	850	91.2	874	3	US-09-051-696-4	Sequence 4, Appl
14	842.4	90.4	930	2	US-08-029-022-2	Sequence 2, Appli
15	842.4	90.4	930	2	US-08-029-022-4	Sequence 4, Appli
16	842.4	90.4	930	2	US-08-246-376-2	Sequence 2, Appli
17	842.4	90.4	930	2	US-08-246-376-4	Sequence 4, Appli
18	842.4	90.4	930	2	US-07-972-135-2	Sequence 2, Appli
19	842.4	90.4	930	2	US-07-972-135-4	Sequence 4, Appli
20	842.4	90.4	930	2	US-08-256-004-2	Sequence 2, Appli
21	842.4	90.4	930	3	US-09-006-841-2	Sequence 2, Appli
22	842.4	90.4	930	3	US-09-006-841-4	Sequence 4, Appli
23	842.4	90.4	930	3	US-09-461-686-2	Sequence 2, Appli
24	842.4	90.4	930	3	US-09-132-391-2	Sequence 2, Appli
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26	842.4	90.4	930	3	US-09-090-030-2	Sequence 2, Appli
27	842.4	90.4	930	3	US-09-090-030-4	Sequence 4, Appli
28	842.4	90.4	930	6	PCT-US93-05366-2	Sequence 2, Appli
29	842.4	90.4	930	6	PCT-US93-05366-4	Sequence 4, Appli
30	810	86.9	4326	3	US-08-760-615-7	Sequence 7, Appli
31	807.4	86.6	4276	3	US-09-721-480-1	Sequence 1, Appli
32	807.4	86.6	5128	3	US-09-721-480-2	Sequence 2, Appli
33	807.4	86.6	5459	3	US-09-721-480-4	Sequence 4, Appli
34	801	85.9	5882	3	US-09-721-480-6	Sequence 6, Appli
35	801.4	86.0	9600	3	US-08-910-647-1	Sequence 1, Appli
36	801.4	86.0	9600	3	US-08-910-925-1	Sequence 1, Appli
37	801	85.9	4328	3	US-08-132-808-1	Sequence 1, Appli
38	801	85.9	4328	3	US-09-620-925-1	Sequence 1, Appli
39	801	85.9	4328	3	US-09-620-925-2	Sequence 2, Appli
40	801	85.9	4328	3	US-09-620-260-1	Sequence 1, Appli
41	801	85.9	4328	3	US-09-620-259-1	Sequence 1, Appli
42	801	85.9	4818	3	US-08-910-647-4	Sequence 4, Appli
43	801	85.9	4818	3	US-08-910-925-4	Sequence 4, Appli
44	801	85.9	5107	3	US-08-910-647-3	Sequence 3, Appli
45	801	85.9	5107	3	US-09-620-925-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1.
US-08-276-852-156
; Sequence 156, Application US/08276852
Patent No. 5652138

GENERAL INFORMATION:
; Patent No. 5652138
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 13254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double